1. List of probesets upregulated in 4T1-derived tumors grown in preirradiated *vs.* nonirradiated stroma

Probeset ID (Affymetrix®)	logFC	Average expression	t	P value	B	Chromo	Start	End	Strand	Gene ID	Gene name	Gene description	Location (Ingenuity®)
10490913	2.18	8.5363	2.36	0.0442	-3.62	chr3	1.49E+07	1.49E+07	+	NM_007606	Car3	carbonic anhydrase 3	Cytoplasm
10398075	1.46	8.2283	2.48	0.0365	-3.46	chr12	1.06E+08	1.06E+08	+	NM_009252	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	Extracellular Space
10599736	1.35	7.1345	2.28	0.0497	-3.71	chrX	5.40E+07	5.40E+07	+	NM_001077361	Fhl1	four and a half LIM domains 1	Cytoplasm
10559200	1.12	8.7379	2.30	0.0483	-3.69	chr7	1.50E+08	1.50E+08	+	NM_009405	Tnni2	troponin I, skeletal, fast 2	Cytoplasm
10358476	1.07	6.3238	2.58	0.0306	-3.32	chr1	1.52E+08	1.52E+08	-	NM_021400	Prg4	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein	Extracellular Space
10352838	1.04	7.9531	4.10	0.0030	-1.49	chr1	1.95E+08	1.95E+08	+	NM_008484	Lamb3	laminin, beta 3	Extracellular Space
10494160	1.00	5.9723	2.39	0.0419	-3.57	chr3	9.49E+07	9.49E+07	+	NM_016712	Tmod4	tropomodulin 4	Cytoplasm
10391052	0.87	7.2999	3.10	0.0135	-2.66	chr11	1.00E+08	1.00E+08	-	NM_016958	Krt14	keratin 14	Cytoplasm
10570663	0.85	7.9282	3.93	0.0038	-1.68	chr8	2.22E+07	2.22E+07	+	NM_007849	Defa25	defensin, alpha, 25	Extracellular Space
10458894	0.80	9.0899	3.53	0.0070	-2.14	chr18	5.27E+07	5.27E+07	-	NM_010728	Lox	lysyl oxidase	Extracellular Space
10487040	0.76	9.2208	9.12	0.0000	1.90	chr2	1.25E+08	1.25E+08	-	NM_007993	Fbn1	fibrillin 1	Extracellular Space
10541496	0.76	8.8686	6.48	0.0001	0.57	chr6	1.22E+08	1.22E+08	+	NM_015776	Mfap5	microfibrillar associated protein 5	Extracellular Space
10435948	0.75	8.7805	4.82	0.0011	-0.76	chr16	4.51E+07	4.51E+07	+	NM_026439	Ccdc80	coiled-coil domain containing 80	Nucleus
10601659	0.73	6.8825	6.55	0.0001	0.61	chrX	1.30E+08	1.30E+08	+	NM_026838	Srpx2	sushi-repeat-containing protein, X-linked 2	Cytoplasm
10374083	0.73	8.7103	4.65	0.0014	-0.92	chr11	5.76E+06	5.77E+06	+	NM_009636	Aebp1	AE binding protein 1	Nucleus
10358787	0.70	10.0552	3.25	0.0106	-2.47	chr1	1.55E+08	1.55E+08	-	NM_008485	Lamc2	laminin, gamma 2	Extracellular Space
10508719	0.69	8.5345	2.83	0.0207	-3.01	chr4	1.32E+08	1.32E+08	+	NR_029412	Snora16a	small nucleolar RNA, H/ACA box 16A	Unknown
10410931	0.68	8.0667	4.28	0.0023	-1.30	chr13	8.98E+07	8.99E+07	-	NM_001081249	Vcan	versican	Extracellular Space
10350173	0.68	9.9907	5.69	0.0004	0.00	chr1	1.38E+08	1.38E+08	+	NM_001130174	Tnnt2	troponin T2, cardiac	Cytoplasm
10431564	0.67	6.1379	2.48	0.0362	-3.46	chr15	8.92E+07	8.93E+07	-	NM_009948	Cpt1b	carnitine palmitoyltransferase 1b, muscle	Cytoplasm
10534667	0.65	10.3218	3.14	0.0126	-2.61	chr5	1.38E+08	1.38E+08	-	NM_008871	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	Extracellular Space
10513739	0.63	11.2692	7.38	0.0001	1.11	chr4	6.36E+07	6.37E+07	-	NM_011607	Tnc	tenascin C	Extracellular Space
10415857	0.61	7.4739	4.40	0.0019	-1.17	chr14	6.41E+07	6.41E+07	+	NM_177628	Fam167a	family with sequence similarity 167, member A	Unknown
10346015	0.61	9.7365	4.71	0.0013	-0.86	chr1	4.54E+07	4.54E+07	+	NM_009930	Col3a1	collagen, type III, alpha 1	Extracellular Space
10518147	0.61	8.8723	2.49	0.0357	-3.44	chr4	1.43E+08	1.43E+08	-	NM_010329	Pdpn	podoplanin	Plasma Membrane
10487937	0.60	6.3615	4.91	0.0010	-0.67	chr2	1.32E+08	1.32E+08	-	NM_144944	Prokr2	prokineticin receptor 2	Plasma Membrane
10583090	0.59	7.2278	3.44	0.0079	-2.25	chr9	7.50E+06	7.51E+06	+	NM_019471	Mmp10	matrix metallopeptidase 10	Extracellular Space
10438904	0.58	9.3375	3.74	0.0050	-1.89	chr16	3.03E+07	3.03E+07	-	NM_028973	Lrrc15	leucine rich repeat containing 15	Plasma Membrane
10435641	0.58	9.4378	4.95	0.0009	-0.64	chr16	3.78E+07	3.78E+07	+	NM_008047	Fstl1	follistatin-like 1	Extracellular Space
10485948	0.57	6.6886	3.87	0.0041	-1.74	chr2	1.14E+08	1.14E+08	-	NM_011824	Grem1	gremlin 1	Extracellular Space
10359624	0.55	8.2766	5.00	0.0009	-0.59	chr1	1.65E+08	1.65E+08	-	NM_175686	Prrx1	paired related homeobox 1	Nucleus
10594066	0.55	8.4434	5.82	0.0003	0.10	chr9	5.81E+07	5.82E+07	-	NM_010729	Loxl1	lysyl oxidase-like 1	Extracellular Space
10492798	0.55	9.1347	3.37	0.0089	-2.34	chr3	8.36E+07	8.36E+07	+	NM_009144	Sfrp2	secreted frizzled-related protein 2	Extracellular Space
10354309	0.55	7.6672	7.53	0.0000	1.19	chr1	4.54E+07	4.56E+07	-	NM_007737	Col5a2	collagen, type V, alpha 2	Extracellular Space
10451932	0.54	6.1282	2.39	0.0421	-3.58	chr17	5.62E+07	5.62E+07	-	NM_020568	Plin4	perilipin 4	Cytoplasm
10536220	0.54	11.0293	5.83	0.0003	0.10	chr6	4.46E+06	4.49E+06	+	NM_007743	Col1a2	collagen, type I, alpha 2	Extracellular Space
10356520	0.52	9.3982	4.55	0.0016	-1.03	chr1	9.27E+07	9.27E+07	-	AF064749	Col6a3	collagen, type VI, alpha 3	Extracellular Space
10447649	0.52	6.8439	4.36	0.0021	-1.22	chr17	7.93E+06	7.97E+06	-	NM_001081416	Fndc1	fibronectin type III domain containing 1	Plasma Membrane
10513208	0.52	7.5158	2.91	0.0182	-2.90	chr4	5.81E+07	5.82E+07	-	NM_022814	Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	Cytoplasm
10593723	0.52	8.3038	4.36	0.0021	-1.22	chr9	5.45E+07	5.45E+07	-	NM_053178	Acsbg1	acyl-CoA synthetase bubblegum family member 1	Cytoplasm
10375175	0.51	8.3911	3.54	0.0068	-2.12	chr11	3.49E+07	3.55E+07	+	NM_011412	Slit3	slit homolog 3 (Drosophila)	Extracellular Space
10416215	0.50	8.0337	5.07	0.0008	-0.52	chr14	7.00E+07	7.01E+07	+	NM_033325	Loxl2	lysyl oxidase-like 2	Extracellular Space
10447951	0.50	10.3232	5.25	0.0006	-0.37	chr17	1.48E+07	1.48E+07	-	NM_011581	Thbs2	thrombospondin 2	Extracellular Space
10380419	0.49	11.5944	5.59	0.0004	-0.08	chr11	9.48E+07	9.48E+07	+	NM_007742	Col1a1	collagen, type I, alpha 1	Extracellular Space
10487994	0.49	8.2408	2.51	0.0347	-3.42	chr2	1.33E+08	1.33E+08	-	NM_198029	Fermt1	fermitin family homolog 1 (Drosophila)	Plasma Membrane

10568536	0.49	7.9738	6.02	0.0002	0.25	chr7	1.39E+08	1.39E+08	-	NM_018867	Cpxm2	carboxypeptidase X 2 (M14 family)	Extracellular Space
10498383	0.48	6.4482	3.39	0.0086	-2.31	chr3	5.91E+07	5.91E+07	-	NM_001162884	Igsf10	immunoglobulin superfamily, member 10	Extracellular Space
10344897	0.48	7.2176	3.93	0.0038	-1.68	chr1	1.27E+07	1.29E+07	+	NM_172294	Sulf1	sulfatase 1	Cytoplasm
10440534	0.48	5.8792	2.99	0.0160	-2.80	chr16	8.59E+07	8.59E+07	-	NM_011782	Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	Extracellular Space
10568668	0.47	6.9459	6.19	0.0002	0.37	chr7	1.41E+08	1.41E+08	-	NM_007400	Adam12	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	Plasma Membrane
10581013	0.47	8.1514	2.98	0.0164	-2.82	chr8	1.05E+08	1.05E+08	-	NM_009866	Cdh11	cadherin 11	Plasma Membrane
10593123	0.47	7.5068	5.99	0.0002	0.22	chr9	4.57E+07	4.57E+07	-	NM_011526	Tagln	transgelin	Cytoplasm
10388430	0.47	9.2110	4.60	0.0015	-0.97	chr11	7.52E+07	7.52E+07	-	NM_011340	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	Extracellular Space
10549964	0.47	5.9084	2.77	0.0227	-3.08	chr7	1.16E+07	1.16E+07	+	NM_001013765	Zscan4c	zinc finger and SCAN domain containing 4C	Nucleus
10436487	0.47	6.4848	5.41	0.0005	-0.24	chr16	6.58E+07	6.59E+07	+	NM_028572	Vgll3	vestigial like 3 (Drosophila)	Nucleus
10412267	0.46	9.6762	2.89	0.0187	-2.92	chr13	1.16E+08	1.16E+08	-	NM_008396	Itga2	integrin alpha 2	Plasma Membrane
10563077	0.46	8.7372	2.72	0.0246	-3.14	chr7	5.23E+07	5.23E+07	-	NM_026555	Rcn3	reticulocalbin 3, EF-hand calcium binding domain	Cytoplasm
10487645	0.46	7.4009	2.32	0.0468	-3.66	chr2	1.30E+08	1.30E+08	-	NM_019696	Cpxm1	carboxypeptidase X 1 (M14 family)	Extracellular Space
10368289	0.46	9.2840	2.51	0.0348	-3.42	chr10	2.44E+07	2.44E+07	-	NM_008813	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	Plasma Membrane
10496405	0.46	6.0684	2.36	0.0438	-3.61	chr3	1.38E+08	1.38E+08	+	NM_177860	Gm5105	predicted gene 5105	Unknown
10469151	0.45	6.3380	2.44	0.0385	-3.51	chr2	1.01E+07	1.02E+07	+	NM_172471	Itih5	inter-alpha (globulin) inhibitor H5	Extracellular Space
10443494	0.45	6.3695	2.53	0.0335	-3.39	chr17	2.95E+07	2.95E+07	+	NM_023734	Pi16	peptidase inhibitor 16	Extracellular Space
10500808	0.45	9.6446	3.49	0.0073	-2.18	chr3	1.04E+08	1.04E+08	-	NM_133859	Olfml3	olfactomedin-like 3	Extracellular Space
10375614	0.44	6.3189	3.09	0.0137	-2.68	chr11	4.96E+07	4.97E+07	+	NM_013529	Gfpt2	glutamine fructose-6-phosphate transaminase 2	Cytoplasm
10585803	0.44	8.8754	4.67	0.0013	-0.90	chr9	5.80E+07	5.80E+07	+	NM_009291	Stra6	stimulated by retinoic acid gene 6	Plasma Membrane
10606369	0.44	7.2207	4.96	0.0009	-0.63	chrX	1.05E+08	1.05E+08	-	NM_008409	Itm2a	integral membrane protein 2A	Plasma Membrane
10598976	0.44	10.4754	3.67	0.0056	-1.98	chrX	2.04E+07	2.05E+07	+	NM_001044384	Timp1	tissue inhibitor of metalloproteinase 1	Extracellular Space
10595211	0.44	10.3784	4.13	0.0029	-1.46	chr9	7.94E+07	7.96E+07	-	NM_007730	Col12a1	collagen, type XII, alpha 1	Extracellular Space
10467124	0.43	10.2560	5.61	0.0004	-0.07	chr19	3.43E+07	3.43E+07	-	NM_007392	Acta2	actin, alpha 2, smooth muscle, aorta	Cytoplasm
10453939	0.43	6.2555	3.60	0.0063	-2.06	chr18	1.25E+07	1.27E+07	+	NM_010680	Lama3	laminin, alpha 3	Extracellular Space
10417887	0.42	5.5150	2.35	0.0446	-3.62	chr14	2.13E+07	2.13E+07	-	NM_029104	Zmynd17	zinc finger, MYND domain containing 17	Unknown
10355813	0.41	6.9405	5.68	0.0004	-0.01	chr1	7.52E+07	7.53E+07	-	NM_008985	Ptprn	protein tyrosine phosphatase, receptor type, N	Plasma Membrane
10369844	0.41	7.2783	3.72	0.0052	-1.92	chr10	7.04E+07	7.06E+07	-	NM_031397	Bicc1	bicaudal C homolog 1 (Drosophila)	Cytoplasm
10424140	0.41	8.2220	4.91	0.0010	-0.68	chr15	5.51E+07	5.54E+07	+	NM_181277	Col14a1	collagen, type XIV, alpha 1	Extracellular Space
10584561	0.41	6.6913	4.17	0.0027	-1.42	chr9	4.05E+07	4.06E+07	+	NM_133733	9030425E11Rik	RIKEN cDNA 9030425E11 gene	Plasma Membrane
10454172	0.41	7.4595	2.30	0.0482	-3.69	chr18	2.07E+07	2.08E+07	+	NM_007883	Dsg2	desmoglein 2	Plasma Membrane
10359307	0.41	6.1051	3.46	0.0077	-2.22	chr1	1.62E+08	1.62E+08	-	NM_177839	Tnn	tenascin N	Extracellular Space
10583071	0.40	8.5022	2.65	0.0274	-3.23	chr9	7.45E+06	7.46E+06	+	NM_010809	Mmp3	matrix metallopeptidase 3	Extracellular Space
10416406	0.40	7.2044	3.53	0.0070	-2.14	chr14	7.50E+07	7.51E+07	+	NM_172812	Htr2a	5-hydroxytryptamine (serotonin) receptor 2A	Plasma Membrane
10456653	0.40	5.9761	4.20	0.0026	-1.38	chr18	7.46E+07	7.49E+07	+	NM_201600	Myo5b	myosin VB	Cytoplasm
10491699	0.40	6.3274	3.82	0.0045	-1.80	chr3	3.72E+07	3.73E+07	+	NM_008006	Fgf2	fibroblast growth factor 2	Extracellular Space
10485117	0.40	7.7068	3.31	0.0097	-2.41	chr2	9.18E+07	9.19E+07	-	NM_011957	Creb3l1	cAMP responsive element binding protein 3-like 1	Nucleus
10563377	0.40	7.3611	4.23	0.0025	-1.35	chr7	5.30E+07	5.30E+07	-	NM_017465	Sult2b1	sulfotransferase family, cytosolic, 2B, member 1	Cytoplasm
10423379	0.40	7.1270	2.64	0.0282	-3.26	chr15	2.74E+07	2.74E+07	+	AF075717	Tiaf2	TGF-beta1-induced anti-apoptotic factor 2	Nucleus
10403834	0.40	5.1177	2.82	0.0210	-3.02	chr13	1.97E+07	1.98E+07	+	NM_016687	Sfrp4	secreted frizzled-related protein 4	Extracellular Space
10414065	0.39	7.9886	3.73	0.0052	-1.91	chr14	3.49E+07	3.49E+07	+	NM_013473	Anxa8	annexin A8	Plasma Membrane
10427052	0.39	10.5278	4.92	0.0009	-0.66	chr15	1.01E+08	1.01E+08	+	NM_033073	Krt7	keratin 7	Cytoplasm
10500938	0.39	6.6543	6.31	0.0002	0.45	chr3	1.05E+08	1.05E+08	-	NM_009520	Wnt2b	wingless related MMTV integration site 2b	Extracellular Space
10472050	0.39	5.8919	3.29	0.0100	-2.43	chr2	5.19E+07	5.19E+07	+	NM_009398	Tnfaip6	tumor necrosis factor alpha induced protein 6	Extracellular Space
10600169	0.39	11.4083	3.06	0.0144	-2.72	chrX	7.07E+07	7.07E+07	+	NM_007542	Bgn	biglycan	Extracellular Space
10345824	0.39	5.9312	5.74	0.0003	0.04	chr1	4.06E+07	4.06E+07	+	NM_010553	Il18rap	interleukin 18 receptor accessory protein	Plasma Membrane
10423109	0.38	7.7785	4.93	0.0009	-0.66	chr15	1.10E+07	1.13E+07	+	NM_175501	Adamts12	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	Extracellular Space
10381898	0.38	7.4551	3.63	0.0060	-2.03	chr11	1.05E+08	1.05E+08	+	NM_008626	Mrc2	mannose receptor, C type 2	Plasma Membrane

10597531	0.38	7.0730	5.57	0.0004	-0.10	chr9	1.16E+08	1.17E+08	-	NM_001172123	Rbms3	RNA binding motif, single stranded interacting protein	Cytoplasm

2. List of probesets downregulated in 4T1-derived tumors grown in preirradiated *vs.* nonirradiated stroma

Probeset ID (Affymetrix®)	logFC	Average expression	t	P value	B	Chrom	Start	End	Strand	Gene ID	Gene name	Gene description	Location (Ingenuity®)
10420295	-1.09	7.9839	-2.46	0.0373	-3.48	chr14	5.68E+07	5.69E+07	-	NM_010374	Gzmf	granzyme F	Cytoplasm
10417526	-0.87	7.3350	-2.36	0.0439	-3.61	chr14	8.80E+06	8.83E+06	-	NM_007870	Dnase1l3	deoxyribonuclease 1-like 3	Nucleus
10363475	-0.82	7.5521	-3.34	0.0092	-2.36	chr10	6.08E+07	6.08E+07	+	NM_011073	Prf1	perforin 1 (pore forming protein)	Cytoplasm
10397882	-0.77	7.7243	-7.55	0.0000	1.20	chr12	1.04E+08	1.04E+08	+	NM_007693	Chga	chromogranin A	Cytoplasm
10445758	-0.66	8.6105	-3.08	0.0140	-2.69	chr17	4.84E+07	4.84E+07	+	NM_001033922	Treml4	triggering receptor expressed on myeloid cells-like 4	Unknown
10492229	-0.65	7.3829	-7.06	0.0001	0.93	chr3	5.88E+07	5.89E+07	+	NM_016738	Rpl13	ribosomal protein L13	Cytoplasm
10384448	-0.64	7.1933	-2.38	0.0427	-3.59	chr11	1.64E+07	1.64E+07	-	NM_011343	Sec61g	SEC61, gamma subunit	Plasma Membrane
10569020	-0.63	7.8228	-2.64	0.0280	-3.25	chr7	1.48E+08	1.48E+08	-	NM_001033632	Ifitm6	interferon induced transmembrane protein 6	Plasma Membrane
10534493	-0.60	7.4592	-3.53	0.0070	-2.14	chr5	1.36E+08	1.36E+08	-	NM_019577	Ccl24	chemokine (C-C motif) ligand 24	Extracellular Space
10496539	-0.58	7.1705	-2.62	0.0287	-3.27	chr3	1.42E+08	1.42E+08	+	NM_153564	Gbp5	guanylate binding protein 5	Plasma Membrane
10447354	-0.58	7.6417	-3.87	0.0042	-1.75	chr17	8.75E+07	8.75E+07	+	NM_025868	Tmx2	thioredoxin-related transmembrane protein 2	Nucleus
10377774	-0.57	8.3329	-4.61	0.0015	-0.97	chr11	6.99E+07	7.00E+07	+	NM_145137	Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2	Plasma Membrane
10401841	-0.55	7.3111	-2.36	0.0439	-3.61	chr12	9.20E+07	9.20E+07	-	NM_010050	Dio2	deiodinase, iodothyronine, type II	Cytoplasm
10375472	-0.55	6.4460	-5.36	0.0005	-0.27	chr11	4.66E+07	4.67E+07	+	NM_178759	Timd4	T-cell immunoglobulin and mucin domain containing 4	Plasma Membrane
10589535	-0.54	7.6081	-2.56	0.0318	-3.35	chr9	1.10E+08	1.10E+08	+	NM_008694	Ngp	neutrophilic granule protein	Extracellular Space
10453057	-0.53	7.4524	-4.25	0.0024	-1.33	chr17	8.01E+07	8.01E+07	-	NM_009994	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	Cytoplasm
10566026	-0.52	9.0038	-2.51	0.0344	-3.42	chr7	1.09E+08	1.09E+08	-	NM_008035	Folr2	folate receptor 2 (fetal)	Plasma Membrane
10448124	-0.52	7.2692	-4.72	0.0012	-0.85	chr17	1.80E+07	1.80E+07	-	NM_013521	Fpr1	formyl peptide receptor 1	Plasma Membrane
10379530	-0.51	7.4384	-3.47	0.0076	-2.21	chr11	8.19E+07	8.19E+07	+	NM_011331	Ccl12	chemokine (C-C motif) ligand 12	Extracellular Space
10379633	-0.50	8.4463	-3.86	0.0043	-1.76	chr11	8.29E+07	8.31E+07	+	NM_011407	Slfn1	schlafen 1	Nucleus
10587799	-0.50	6.5713	-3.23	0.0110	-2.50	chr9	9.22E+07	9.22E+07	+	NM_008880	Plscr2	phospholipid scramblase 2	Cytoplasm
10548817	-0.50	9.2673	-3.11	0.0132	-2.65	chr6	1.37E+08	1.37E+08	-	NM_025806	Plbd1	phospholipase B domain containing 1	Extracellular Space
10587315	-0.48	8.6745	-3.58	0.0065	-2.08	chr9	7.80E+07	7.81E+07	+	NM_010357	Gsta4	glutathione S-transferase, alpha 4	Cytoplasm
10474915	-0.47	8.5734	-3.02	0.0153	-2.76	chr2	1.19E+08	1.19E+08	+	NM_177157	Gchfr	GTP cyclohydrolase I feedback regulator	Cytoplasm
10389207	-0.45	8.4413	-2.88	0.0192	-2.95	chr11	8.33E+07	8.33E+07	-	NM_013653	Ccl5	chemokine (C-C motif) ligand 5	Extracellular Space
10430811	-0.45	6.4848	-3.09	0.0137	-2.68	chr15	8.19E+07	8.19E+07	-	NM_011482	Nhp2l1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	Nucleus
10428376	-0.44	8.6205	-2.85	0.0200	-2.98	chr15	4.23E+07	4.25E+07	-	NM_009640	Angpt1	angiopoietin 1	Extracellular Space
10410766	-0.44	8.3904	-4.48	0.0017	-1.09	chr13	7.83E+07	7.83E+07	-	NM_010151	Nr2f1	nuclear receptor subfamily 2, group F, member 1	Nucleus
10355984	-0.43	10.1000	-2.95	0.0170	-2.85	chr1	7.98E+07	7.99E+07	-	NM_009255	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	Extracellular Space
10475487	-0.42	6.7154	-2.80	0.0218	-3.05	chr2	1.22E+08	1.22E+08	+	NM_172980	Slc28a2	solute carrier family 28 (sodium-coupled nucleoside transporter), member	Plasma Membrane
10414548	-0.42	6.5233	-2.41	0.0406	-3.55	chr14	5.17E+07	5.18E+07	+	NM_030098	Rnase6	ribonuclease, RNase A family, 6	Extracellular Space
10518453	-0.42	6.2405	-3.92	0.0038	-1.68	chr4	1.47E+08	1.47E+08	-	NM_024166	Chchd2	coiled-coil-helix-coiled-coil-helix domain containing 2	Cytoplasm
10359689	-0.41	8.6429	-3.46	0.0078	-2.23	chr1	1.66E+08	1.66E+08	-	NM_009721	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	Plasma Membrane
10502335	-0.41	6.1184	-3.14	0.0126	-2.61	chr3	1.36E+08	1.36E+08	-	NM_001033350	Bank1	B-cell scaffold protein with ankyrin repeats 1	Extracellular Space
10601044	-0.40	7.2187	-2.78	0.0225	-3.07	chrX	9.79E+07	9.79E+07	+	NM_023608	Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	Plasma Membrane
10604844	-0.40	8.6203	-2.37	0.0429	-3.59	chrX	6.00E+07	6.00E+07	-	NM_009214	Sms	spermine synthase	Cytoplasm
10423654	-0.40	8.2834	-3.11	0.0132	-2.65	chr15	3.52E+07	3.52E+07	+	NM_054049	Osr2	odd-skipped related 2 (Drosophila)	Nucleus
10476945	-0.39	6.6524	-2.33	0.0464	-3.66	chr2	1.50E+08	1.50E+08	+	NM_009977	Cst7	cystatin F (leukocystatin)	Extracellular Space
10404069	-0.39	8.4806	-3.13	0.0129	-2.63	chr13	2.39E+07	2.39E+07	+	NM_030609	Hist1h1a	histone cluster 1, H1a	Nucleus
10548375	-0.39	8.8023	-2.63	0.0286	-3.27	chr6	1.29E+08	1.29E+08	-	NM_020008	Clec7a	C-type lectin domain family 7, member a	Plasma Membrane
10434698	-0.38	6.1489	-2.37	0.0434	-3.60	chr16	2.29E+07	2.29E+07	+	NM_021564	Fetub	fetuin beta	Extracellular Space